

Fri Mar 2 09:30:23 2001

us-09-331-631a-5_copy_76_144.rag

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:47:15 ; Search time 210.42 Seconds

(without alignments)

11.213 Million cell updates/sec

Title: US-09-331-631A-5_COPY_76_144
Sequence: 1 NR0RDPQQEQEQCCKRCGR.....EEQREDEKYEERKESDN 69

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: A-Geneseq_36:*
2: /SIDS1/gcgdata/geneseq/geneseq/AA1980.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq/AA1981.DAT:*
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19: /SIDS1/gcgdata/geneseq/geneseq/AA1997.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseq/AA1998.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
1	381	100.0	625	19	W62830
2	363	95.3	666	19	W62828
3	359	94.2	666	19	W62829
4	173	45.4	525	13	W62831
5	173	45.4	566	13	R20181
6	152.5	40.0	590	19	W62832
7	103	27.0	1898	20	W62832
8	102	26.8	1162	21	Y30795
9	97.5	25.6	1135	21	Y38500
10	97.5	25.6	1233	21	Y68784
11	97.5	25.6	1239	20	Y55954
12	97	25.5	482	20	Y55931
					Y07067

13	97	25.5	1297		
14	96	25.2	1360		
15	95.5	25.1	1326		
16	95	24.9	444	20	
17	95	24.9	524	20	
18	94.5	24.8	611	20	
19	93	24.4	2023	21	
20	93	24.4	2074	21	
21	90.5	23.8	409	20	
22	90.5	23.8	489	20	
23	89	23.4	346	20	
24	89	23.4	373	20	
25	88	23.1	593	19	
26	88	23.1	1197	21	
27	88	23.1	1658	21	
28	86.5	22.7	562	16	
29	85.5	22.4	740	13	
30	85.5	22.4	740	13	
31	85	22.3	910	20	
32	85	22.3	1214	21	
33	85	22.3	1715	21	
34	84.5	22.2	1299	21	
35	84	22.0	200	18	
36	84	22.0	200	18	
37	84	22.0	200	18	
38	84	22.0	200	18	
39	83.5	21.9	1382	18	
40	83.5	21.9	303	15	
41	83.5	21.9	326	20	
42	82.5	21.7	432	20	
43	82	21.5	301	8	
44	82	21.5	648	20	
45	82	21.5	1144	20	

ALIGNMENTS

RESULT 1	W62830	standard: Protein; 625 AA.
ID	W62830	
AC	W62830	
XX		
DT	27-OCT-1998	(first entry)
XX		
DE	Macadamia integrifolia antimicrobial protein.	
XX		
KM	antimicrobial protein; infestation; control.	
XX		
OS	Macadamia integrifolia.	
XX		
EH	Key	Location/Qualifiers
FT	Peptide	1..28
FT	Protein	/note="signal peptide"
FT		29..666
XX		/note="mature protein"
PN	W09827805-A1.	
XX		
PD	02-JUL-1998.	
XX		
PE	22-DEC-1997;	97WO-AU00874.
XX		
PR	20-DEC-1996;	96AU-0004275.
XX		
PA	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.	
XX		
PI	Bower NI, Coulter KC, Green JL, Manners JM, Marcus JP;	
DR	WPI: 1998-372729/32.	
XX	N-PSDB: V42316.	
XX		


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M62831
ID W62831 standard; Protein: 525 AA.
AC
XX W62831;
XX
XX
XX 27-OCT-1998 (first entry)
XX
XX Theobroma cacao antimicrobial protein.
XX antimicrobial protein; infestation; control.
XX
XX Theobroma cacao.
XX
XX WO9827805-A1.
XX
XX 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-AU00874.
XX
XX 20-DEC-1996; 96AU-0004275.
XX
XX (REFR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
XX
XX WPI; 1998-377279/32.
XX
XX Novel anti-microbial protein from e.g. Macadamia integrifolia -
XX useful for controlling microbial infestations of plants or mammals
XX
XX Claim 1: Page 47-49; 96pp; English.
XX
XX The sequence is that of an antimicrobial protein which can
XX be used to control microbial infestations in plants and mammalian
XX animals.
XX
XX Sequence 525 AA;
XX
SQ
Query Match 45.4%; Score 173; DB 19; Length 525;
Best Local Similarity 32.6%; Pred. No. 6.7e-10;
Matches 31; Conservative 17; Mismatches 15; Indels 32; Gaps 1;
QY 3 QRDPOOQYEOCCRCORRETEPRHMOICQRCERRRERKRRKQO----- 46
DB 35 erdpqrqyegqqrccseateereqegqecrercerykeqqrqgeelqryqgqgqrge 94
QY 47 -----KRYEQOREDEEKYEERMK 65
DB 95 qggqgqregqgqqrckweqykeqgergehenyhnkk 129
RESULT 5
R20181
ID R20181 standard; Protein: 566 AA.
XX
XX R20181;
XX
XX 16-APR-1992 (first entry)
XX
XX Sequence encoded by 67 kD T. cacao protein cDNA.
XX
XX Cocoa; flavour; vicillin; seed storage protein.
XX
XX Theobroma cacao.
XX
XX WO9119801-A.
XX
XX 26-DEC-1991.
XX
XX 07-JUN-1991; 91WO-GB00914.
XX
XX 11-JUN-1990; 90GB-0013016.

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XX
XX (MRS) MARS UK LTD.
XX
XX Spencer ME, Hodge R, Deakin EA, Ashton S;
XX
XX WPI; 1992-024418/03.
XX
XX N-PSDB; Q20377.
XX
XX Recombinant cocoa proteins - are responsible for flavour in cocoa
XX beans and produced in large quantities using yeast and bacterial
XX expression vectors
XX
XX Claim 4; Fig 2; 59pp; English.
XX
XX The inventors claim a 67 kD and 31 kD T. cacao protein, and
XX fragments, and encoding DNAs. The 47 kD and 31 kD proteins are
XX derived from the 67 kD precursor. T. cacao protein cDNA was
XX detected in a cDNA library prepared from immature cocoa beans RNA
XX using a probe based on the AA sequence of a CNBr peptide common to
XX the 47 kD and 31 kD polypeptides. Homology searches revealed close
XX homologies between the 67 kD polypeptide and the vicilins, which are
XX seed storage proteins.
XX
XX Sequence 566 AA;
XX
SQ
Query Match 45.4%; Score 173; DB 13; Length 566;
Best Local Similarity 32.6%; Pred. No. 7.2e-10;
Matches 31; Conservative 17; Mismatches 15; Indels 32; Gaps 1;
QY 3 QRDPOOQYEOCCRCORRETEPRHMOICQRCERRRERKRRKQO----- 46
DB 35 erdpqrqyegqqrccseateereqegqecrercerykeqqrqgeelqryqgqgqrge 94
QY 47 -----KRYEQOREDEEKYEERMK 65
DB 95 qggqgqregqgqqrckweqykeqgergehenyhnkk 129
RESULT 6
W62832
ID W62832 standard; Protein: 590 AA.
XX
XX W62832;
XX
XX 27-OCT-1998 (first entry)
XX
XX Gossypium hirsutum antimicrobial protein.
XX
XX antimicrobial protein; infestation; control.
XX
XX Gossypium hirsutum.
XX
XX WO9827805-A1.
XX
XX 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-AU00874.
XX
XX 20-DEC-1996; 96AU-0004275.
XX
XX (REFR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
XX
XX WPI; 1998-377279/32.
XX
XX Novel anti-microbial protein from e.g. Macadamia integrifolia -
XX useful for controlling microbial infestations of plants or mammals
XX
XX Claim 1; Page 49-51; 96pp; English.
XX
XX The sequence is that of an antimicrobial protein which can

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be used to control microbial infestations in plants and mammalian animals.
Sequence 590 AA;

Query Match 40.0%; Score 152.5; DB 19; Length 590;
Best Local Similarity 35.3%; Pred. No. 8.2e-08;
Matches 30; Conservative 18; Mismatches 18; Indels 19; Gaps 2;

QY 1 NRORPDQOQYECOCRCORRETEPRHMOICORCERREYERKRRQOKRYEEOQ----- 53
Db 78 hrpedpqrtyeeccqec--rgeerqgpcqgrclrfegqgqsrqrgecqhchqge 135

QY 54 -----REDEKYEERKMGD 68
Db 136 grpekkgqcyvcrekkygenpwrg 160

RESULT 7
Y30795
ID Y30795 standard; Protein; 1898 AA.
XX
AC Y30795;

DI 25-NOV-1999 (first entry)
XX

DE A human trichohyalin (TRHY) protein.
XX

KM Human; trichohyalin; TRHY; protein; tissue structure; wound healing;
KM terminally differentiating epidermal tissue; proteinaceous gel;
XX breast implant.

OS Homo sapiens.
XX

PN US5958752-A.
XX

PD 28-SEP-1999.
XX

PF 14-FEB-1997; 97US-0800644.
XX

PR 30-APR-1993; 93US-0056200.
XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX

PI Kim I, Chung S, Park S, Steinert PM, Lee S;
XX

DR WPI: 1999-561041/47.
XX

DR N-PSDB: 222301.
XX

PT Human trichohyalin useful for forming a proteinaceous gel that promotes
XX wound healing -

PS Disclosure: Fig 3A-W; 126pp; English.
XX

CC The present sequence represents a human trichohyalin (TRHY) protein.
CC CC The protein is found in terminally differentiating epidermal tissue,
CC and is involved in forming the structural architecture of such
CC tissue. The trichohyalin protein is useful for forming a
CC proteinaceous gel which may then be used for healing wounds, or in
CC breast implants.
XX

CC Sequence 1898 AA;
SQ

Query Match 27.0%; Score 103; DB 20; Length 1898;
Best Local Similarity 31.0%; Pred. No. 0.023;
Matches 22; Conservative 23; Mismatches 20; Indels 6; Gaps 1;

QY 2 RORDPOQOYECOCRCORRETEPRHMOICORCERREYERKRRQOKRYEEOQRE 55
Db 267 rgralqeeegqirklrgerlrrrgeeqqqrllrrrqqllrrkqeeerreeeqe 326

QY 56 DEEKYEERKME 66
Db 327 rregeerreq 337

RESULT 8
Y58500
ID Y58500 standard; Protein; 1162 AA.
XX
AC Y58500;

DT 10-APR-2000 (first entry)
XX

DE HHV8 ORF 73 protein, SEQ ID NO:21.
XX

KM HHV8; detection; diagnosis; Kaposi's sarcoma; AIDS; immunogen;
KM antigen.
XX

OS Human herpesvirus type 8.
XX

FT KEY Location/Qualifiers
FT Misc-difference 96
FT /Label= unknown

PN WO961909-A2.
XX

PD 02-DEC-1999.
XX

PE 26-MAY-1999; 99WO-US11407.
XX

PR 26-MAY-1998; 98US-0086695.
XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX

XX Pau CP;
XX

DR WPI: 2000-097142/08.
XX

PT New methods and compositions for the detection of human herpesvirus -
XX

PS Claim 2; Page 59-62; 68pp; English.
XX

CC Sequences Y58480-Y58532 represent immunogenic polypeptides derived from
CC human herpes virus type 8 (HHV8, a gammaherpesvirus). HHV8 plays an
CC important role in the pathogenesis of AIDS-related Kaposi's sarcoma. The
CC invention relates to a novel method of detecting the presence of human
CC herpesvirus 8 in a biological sample using peptides representative of
CC or more isolated, immunogenic HHV8 peptides with an antibody-containing
CC biological sample, and detecting the formation of a complex between the
CC peptide and the antibody. The presence of a peptide-antibody complex
CC indicates the presence of human herpesvirus 8. The detection of HHV8
CC infection can be used to diagnose AIDS-associated Kaposi's sarcoma. The
CC HHV8-specific antibodies are useful therapeutically when for the passive
CC immunisation of a human against HHV8 infection, thereby reducing HHV8
CC related disease. The detection assays are highly specific, sensitive and
CC accurate. Early detection and treatment of Kaposi's sarcoma could
CC diminish the severity of symptoms related to AIDS and the sensitive
CC techniques could reduce erroneous characterisations of skin disorders.
CC Previous assays for HHV8 antibodies such as immunofluorescence assays,
CC immunoblots and enzyme immunoassays lack the sensitivity and accuracy
CC needed for reliable diagnosis of Kaposi's sarcoma. Further advantages
CC of the assays are that reproducible results are obtained and the method
CC is suitable for rapid throughput and screening of samples economically.
XX

SQ Sequence 1162 AA;

Query Match 26.8%; Score 102; DB 21; Length 1162;
Best Local Similarity 31.3%; Pred. No. 0.017;
Matches 21; Conservative 24; Mismatches 22; Indels 0; Gaps 0;

QY 2 RORDPOQOYECOCRCORRETEPRHMOICORCERREYERKRRQOKRYEEOQREDEKYE 61

[illegible]

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FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	543	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	550	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	554	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	570	
FT	Modified-site	/note=	"potential glycosylation site"
FT	Modified-site	572	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	624	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	625	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	632	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	681	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	682	
FT	Modified-site	/note=	"potential phosphorylation site"
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FT	Modified-site	689	
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FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	718	
FT	Modified-site	/note=	"potential glycosylation site"
FT	Modified-site	720	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	726	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	811	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	815	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Domain	836..1115	
FT	Modified-site	/note=	"NIK1-like kinase domain"
FT	Modified-site	898	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	931	
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FT	Modified-site	958	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	978	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	999	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	1012	
FT	Modified-site	/note=	"potential phosphorylation site"
FT	Modified-site	1067	
FT	Modified-site	/note=	"potential glycosylation site"
FT	Modified-site	1113	
XX	W0200006728-A2.	/note=	"potential phosphorylation site"
XX	10-FEB-2000.		
XX	28-JUL-1999;	99W0-US17132.	
XX	28-JUL-1998;	98US-0123494.	
XX	14-SEP-1998;	98US-0152814.	
PR	14-OCT-1998;	98US-0173482.	
PR	03-NOV-1998;	98US-0106889.	
PR	19-NOV-1998;	98US-0109093.	
PR	22-DEC-1998;	98US-0113796.	
PR	12-JAN-1999;	98US-0173482.	
XX	12-JAN-1999;	99US-0229005.	

KW immunosuppressant.
 XX
 OS Homo sapiens.
 XX
 PN MO9953036-A2.
 XX
 PD 21-OCT-1999.
 XX
 PF 13-APR-1999; 99WO-US08150.
 XX
 PR 14-APR-1998; 98US-0081784.
 XX
 PA (SUGF-) SUGEN INC.
 XX
 PI Plowman G, Martinez R, Whyte D;
 XX
 DR MPI: 1999-611301/52.
 N-PSDB: Z40483.
 XX
 PT Novel kinase-related polypeptides used for the diagnosis and treatment
 of kinase-related diseases and disorders -
 XX
 PS Claim 11: Page 269-274; 387pp; English.
 XX
 CC This sequence represents a novel STE20-related protein kinase. The
 CC invention relates to nucleic acid molecule encoding a kinase polypeptide
 CC selected from STK2, STK3, STK4, STK5, STK6, STK7, ZC1, ZC2, ZC3,
 CC ZC4, KHS2, SUU1, SUU3, GSK2, PAK4 and PAK5. The proteins are used to
 CC identify agonists and antagonists, and to raise antibodies. The
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,
 CC polypeptides, antibodies, antagonists and agonists may be used to treat
 CC diseases such as immune-related disorders and diseases (e.g. Rheumatoid
 CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
 CC rheitis, autoimmunity, and organ transplantation, chronic inflammatory
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative
 CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral
 CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
 CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
 CC mellitus, fibrotic and mesangial disorders. The proteins may also be
 CC useful for cell growth regulation (e.g. in wound healing), T cell
 CC activation, mitosis control, and as immunosuppressants.
 CC
 SQ Sequence 1239 AA:
 XX
 Query Match 25.6%; Score 97.5; DB 20; Length 1239;
 Best Local Similarity 39.2%; Pred. No. 0.051;
 Matches 29; Conservative 17; Mismatches 17; Indels 11; Gaps 4;
 YY 2 RQDPQOQYQOCOK--RCORRETERPHMOICQRCRRYKEKRRK---QOKRYEQOR- 54
 DB 395 rqrriegqkqqrriieeqqrrearrqqrqr--rregeekrrileertrikeeeirr 452
 YY 55 --EDEEKYEERME 66
 DB 453 raeeekrrverege 466
 XX
 RESULT 12
 Y07067 Y07067 standard; Protein: 482 AA.
 AC Y07067;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE Renal cancer associated antigen precursor sequence.
 XX
 KW Cancer associated antigen: diagnosis; research; treatment; human;
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
 KW prostate cancer.

XX
 OS Homo sapiens.
 XX
 PN MO9904265-A2.
 XX
 PD 28-JAN-1999.
 XX
 PF 15-JUL-1998; 98WO-US14679.
 XX
 PR 22-JUN-1998; 98US-0102322.
 PR 17-JUL-1997; 97US-0896164.
 PR 10-OCT-1997; 97US-0061599.
 PR 10-OCT-1997; 97US-0061765.
 PR 10-OCT-1997; 97US-0948705.
 PR 11-OCT-1997; 97GB-0021697.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Chen Y, Gout I, Gure A, O'Hare M, Obata Y, Old LJ;
 PI Pfeundschnuh M, Sahin U, Scanlan MJ, Stockert E;
 PI Tureci O;
 XX
 DR MPI: 1999-132448/11.
 XX
 PT New isolated cancer associated nucleic acids and polypeptides -
 PT isolated using sera from cancer patients, used to develop products
 PT for the diagnosis, monitoring or treatment of cancers
 XX
 PS Disclosure: Page 467-468; 787pp; English.
 XX
 CC The invention relates to a method for diagnosing a disorder characterised
 CC by expression of a human cancer associated antigen precursor coded for by
 CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
 CC biological sample isolated from a subject with an agent that specifically
 CC binds to the NAM, an expression product or a fragment of an expression
 CC product complexed with an HLA molecule; and (b) determining the
 CC interaction between the agent and the NAM or the expression product as a
 CC determination of the disorder. The products and methods can be used in
 CC the diagnosis, monitoring, research, or treatment of conditions
 CC characterised by the expression of various cancer associated antigens.
 CC The invention provides nucleic acid sequences and encoded polypeptides
 CC which are cancer associated antigen precursors expressed in human breast
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 CC lung cancer.
 CC
 SQ Sequence 482 AA:
 XX
 Query Match 25.5%; Score 97; DB 20; Length 482;
 Best Local Similarity 29.7%; Pred. No. 0.022;
 Matches 19; Conservative 25; Mismatches 20; Indels 0; Gaps 0;
 YY 3 QRPDQOQYQOCOKRCORRETERPHMOICQRCRRYKEKRRKQOQRYEQORDEEKEYE 62
 DB 65 ererqrllheawllredkqgefrfkkeekaaakkrgeqerklkqweeqqrkereeeg 124
 YY 63 RMKE 66
 DB 125 krge 128
 XX
 RESULT 13
 Y55932 Y55932 standard; Protein: 1297 AA.
 AC Y55932;
 XX
 DT 18-FEB-2000 (first entry)
 XX
 DE Human ZC2 protein.
 XX
 KW Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;
 KW antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;

